



SEQUENCE LISTING

<110> DYAX Corp.

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Luneau, Christopher J.

Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> 09/884,767

<141> 2001-06-19

<150> US 09/597,321

<151> 2000-06-19

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<170> PatentIn version 3.1

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20 25 30

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35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Gly Ala Gln Ser Asp Gly Gly Ser
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35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys
50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu
65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Ser Glu Gly Gly Ser Glu
85 90 95

Gly Gly Gly Ser Glu Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp
100 105 110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr
115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu
130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg
145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys
180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe
195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln
210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Ser Gly
225 230 235 240

Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly
245 250 255

Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly
260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
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Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
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Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
325 330 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser
420

<210> 214
<211> 957
<212> DNA
<213> Artificial Sequence

<220>
<223> Bacteriophage M13mp18

<400> 214
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ggcacttatac cgccctggta ctagcaaaac cccgctaatac ctaatccttc tcttgaggag 120
tctcagcctc ttaatacttt catgtttcag aataataggt tccgaaatag gcagggggca 180
ttaactgttt atacgggcac tggtaactcaa ggcactgacc ccgttaaaac ttattaccag 240
tacactcctg tatcatcaaa agccatgtat gacgcttact ggaacggtaa attcagagac 300
tgcgctttcc attctggcct taatgaagat ccattcgttt gtgaatatac aggccaatcg 360
tctgacctgc ctcaacctcc tgtcaatgct ggccggcgt ctgggtggc ttctggcgc 420
ggctctgagg gtggcgtggc tgagggtggc gttctgagg gtggcggcgc tgagggaggc 480
ggttccggtg gtggcgtctgg ttccggtgat tttgattatg aaaagatggc aaacgcta 540
aagggggcta tgaccgaaaa tgccgatgaa aacgcgtac agtctgacgc taaaggcaaa 600
cttgattctg tcgctactga ttacggtgct gctatcgatg gttcattgg tgacgtttcc 660
ggccttgcta atggtaatgg tgctactgg gatggctg gctctaattc ccaaattggct 720

caagtcggtg acggtgataa ttcacctta atgaataatt tccgtcaata tttacctcc 780
ctccctcaat cggttgaatg tcgcccttt gtcttagcg ctggtaaacc atatgaattt 840
tctattgatt gtgacaaaat aaacttattc cgtggtgtct ttgcgttct tttatatgtt 900
gccacctta tgtatgtatt ttctacgttt gctaacatac tgcgtataa ggagtct 957

<210> 215
<211> 319
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage M13mp18

<400> 215

Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile
1 5 10 15

Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala
20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met
35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr
50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln
65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly
85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe
100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
115 120 125

Asn Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly
130 135 140

Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly
145 150 155 160

Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
225 230 235 240

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln
245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe
260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn
275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
305 310 315

<210> 216

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Bacteriophage M13mp18

<400> 216
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gaaaacgcgc tacagtctga cgctaaaggc aaacttgatt ctgtcgctac tgattacggt 120

gctgctatcg atggtttcat tggtgacggtt tccggccttg ctaatggtaa tggtgctact 180

ggtgattttg ctggctctaa ttcccaaatg gctcaagtcg gtgacggta taattcacct 240
ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300
tttgtcttta gcgctggtaa accatatgaa ttttctattt attgtgacaa aataaaactta 360
ttccgtggtg tctttgcgtt tctttatat gttgccacct ttatgtatgt atttctacg 420
tttgctaaca tactgcgtaa taaggagtct 450

<210> 217
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacteriophage M13mp18

<400> 217

Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr
1 5 10 15

Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu
20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly
35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro
65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu
115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile
130 135 140

Leu Arg Asn Lys Glu Ser
145 150